

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/590,464
Source: IFWP
Date Processed by STIC: 9/1/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/590,464

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/590,464

DATE: 09/01/2006
TIME: 11:33:27

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\09012006\J590464.raw

*see item 2 on
Ena Summary
Sheet*

3 <110> APPLICANT: Kihara Memorial Yokohama Foundation for the Advancement of Life
Sciences
4 City of Yokohama
6 <120> TITLE OF INVENTION: TRF2 DNA-binding domain mutant proteins, telomeric DNA
mutants, and use
7 of a structure of a complex between a TRF2 DNA binding domain and a double-
8 stranded DNA molecule
10 <130> FILE REFERENCE: FP-047PCT
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/590,464
C--> 13 <141> CURRENT FILING DATE: 2006-08-23
15 <150> PRIOR APPLICATION NUMBER: JP P2004-046238
16 <151> PRIOR FILING DATE: 2004-02-23
18 <160> NUMBER OF SEQ ID NOS: 29
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 189
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(189)
30 <223> OTHER INFORMATION:

see p 3-6

**Does Not Comply
Corrected Diskette Needed**

W--> 32 <400> 1
33 gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa 48
34 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
35 1 5 10 15
37 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
38 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
39 20 25 30
41 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
42 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
43 35 40 45
45 atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
46 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
47 : 50 55 60
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 63
52 <212> TYPE: PRT
53 <213> ORGANISM: Homo sapiens
55 <400> SEQUENCE: 2
57 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
58 1 5 10 15
61 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
62 20 25 30

65 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09012006\J590464.raw

66 35 40 45
69 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
70 50 55 60
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 189
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
78 <220> FEATURE:
79 <223> OTHER INFORMATION: synthetic DNA
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)..(189)
84 <223> OTHER INFORMATION:
W--> 86 <400> 3
87 gaa gac agt aca acc aat ata aca aaa agg cag aag tgg act gta gaa 48
88 Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
89 1 5 10 15
91 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
92 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
93 20 25 30
95 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
96 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
97 35 40 45
99 atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
100 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
101 50 55 60
104 <210> SEQ ID NO: 4
105 <211> LENGTH: 63
106 <212> TYPE: PRT
107 <213> ORGANISM: Artificial
109 <220> FEATURE:
110 <223> OTHER INFORMATION: synthetic DNA
112 <400> SEQUENCE: 4
114 Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
115 1 5 10 15
118 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
119 20 25 30
122 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
123 35 40 45
126 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
127 50 55 60
130 <210> SEQ ID NO: 5
131 <211> LENGTH: 189
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial
135 <220> FEATURE:
136 <223> OTHER INFORMATION: synthetic DNA
138 <220> FEATURE:
139 <221> NAME/KEY: CDS

this is not a DNA sequence

RAW SEQUENCE LISTING

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09012006\J590464.raw

140 <222> LOCATION: (1)..(189)

141 <223> OTHER INFORMATION:

W--> 143 <400> 5

144 gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa 48

145 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

146 1 5 10 15

148 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96

149 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn

150 20 25 30

152 tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144

153 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val

154 35 40 45

156 atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189

157 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn

158 50 55 60

161 <210> SEQ ID NO: 6

162 <211> LENGTH: 63

163 <212> TYPE: PRT

164 <213> ORGANISM: Artificial

166 <220> FEATURE:

167 <223> OTHER INFORMATION: synthetic DNA

not a DNA sequence

169 <400> SEQUENCE: 6

171 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

172 1 5 10 15

175 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn

176 20 25 30

179 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val

180 35 40 45

183 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn

184 50 55 60

187 <210> SEQ ID NO: 7

188 <211> LENGTH: 189

189 <212> TYPE: DNA

190 <213> ORGANISM: Artificial

192 <220> FEATURE:

193 <223> OTHER INFORMATION: synthetic DNA

195 <220> FEATURE:

196 <221> NAME/KEY: CDS

197 <222> LOCATION: (1)..(189)

198 <223> OTHER INFORMATION:

W--> 200 <400> 7

201 gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa 48

202 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu

203 1 5 10 15

205 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96

206 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn

207 20 25 30

209 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144

210 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val

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211 35 40 45
 213 atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
 214 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
 215 50 55 60
 218 <210> SEQ ID NO: 8
 219 <211> LENGTH: 63
 220 <212> TYPE: PRT
 221 <213> ORGANISM: Artificial
 223 <220> FEATURE:
 224 <223> OTHER INFORMATION: synthetic DNA *same env*
 226 <400> SEQUENCE: 8
 228 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
 229 1 5 10 15
 232 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 233 20 25 30
 236 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 237 35 40 45
 240 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
 241 50 55 60
 244 <210> SEQ ID NO: 9
 245 <211> LENGTH: 189
 246 <212> TYPE: DNA
 247 <213> ORGANISM: Artificial
 249 <220> FEATURE:
 250 <223> OTHER INFORMATION: synthetic DNA
 252 <220> FEATURE:
 253 <221> NAME/KEY: CDS
 254 <222> LOCATION: (1)..(189)
 255 <223> OTHER INFORMATION:
 W--> 257 <400> 9
 258 gaa gac agt aca acc aat ata aca aaa aag cag aag tgg act gta gaa 48
 259 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
 260 1 5 10 15
 262 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 263 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 264 20 25 30
 266 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
 267 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
 268 35 40 45
 270 atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
 271 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
 272 50 55 60
 275 <210> SEQ ID NO: 10
 276 <211> LENGTH: 63
 277 <212> TYPE: PRT
 278 <213> ORGANISM: Artificial
 280 <220> FEATURE:
 281 <223> OTHER INFORMATION: synthetic DNA
 283 <400> SEQUENCE: 10

RAW SEQUENCE LISTING

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09012006\J590464.raw

285 Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
 286 1 5 10 15
 289 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 290 20 25 30
 293 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
 294 35 40 45
 297 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
 298 50 55 60

301 <210> SEQ ID NO: 11

302 <211> LENGTH: 189

303 <212> TYPE: DNA

304 <213> ORGANISM: Artificial

306 <220> FEATURE:

307 <223> OTHER INFORMATION: synthetic DNA

309 <220> FEATURE:

310 <221> NAME/KEY: CDS

311 <222> LOCATION: (1)..(189)

312 <223> OTHER INFORMATION:

W--> 314 <400> 11

315 gaa gac agt aca acc aat ata aca aaa agg cag aag tgg act gta gaa 48
 316 Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
 317 1 5 10 15
 319 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 320 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 321 20 25 30
 323 tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
 324 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 325 35 40 45
 327 atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
 328 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
 329 50 55 60

332 <210> SEQ ID NO: 12

333 <211> LENGTH: 63

334 <212> TYPE: PRT

335 <213> ORGANISM: Artificial

337 <220> FEATURE:

338 <223> OTHER INFORMATION: synthetic DNA

340 <400> SEQUENCE: 12

342 Glu Asp Ser Thr Thr Asn Ile Thr Lys Arg Gln Lys Trp Thr Val Glu
 343 1 5 10 15
 346 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 347 20 25 30
 350 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 351 35 40 45
 354 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
 355 50 55 60

358 <210> SEQ ID NO: 13

359 <211> LENGTH: 189

360 <212> TYPE: DNA

same error in Sequence 14

VERIFICATION SUMMARY

DATE: 09/01/2006

PATENT APPLICATION: US/10/590,464

TIME: 11:33:28

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09012006\J590464.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:86 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:84
L:143 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:141
L:200 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:198
L:257 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:255
L:314 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:312
L:371 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:369
L:425 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:423